Madras Agric. J., 100 (4-6): 273-276, June 2013
https://doi.org/10.29321/MAJ.10.001287

Diversity Assessment in Cape Gooseberry (*Physalis peruviana* L.) Genotypes

D.B. Singh*, S. Lal, N. Ahmed, O.C. Sharma, A.A. Pal and A. Mirza
Central Institute of Temperate Horticulture
Old Air Field, PO: Rangreth-190 007, Srinagar, Jammu & Kashmir

Twenty genotypes of Cape gooseberry were evaluated at the experimental field of Central Institute of Temperate Horticulture, Srinagar, for its variability, their interrelationship and diversity pattern based on pomological and chemical traits during 2009 to 2011 by using multivariate analysis. All the genotypes were grouped into four different clusters. Cluster III had the maximum (10) and cluster II had the minimum (2) genotypes. The highest inter cluster distance was observed between I and III. The lowest inter cluster distance was found between the cluster I and IV. Based on cluster mean value, the cluster II was found important for fruits per plant, fruit diameter, low acidity and fruit yield per plant. Cluster I for fruit weight and fruit length. Cluster III for TSS and ascorbic acid and cluster IV for juice content. The parents could be selected accordingly for hybridization programme. Pomological and chemical traits data were also subjected to principal component analysis and the first two principal components axes accounted for 59.04% of the variance among the 20 genotypes. The greater part of variance was accounted for other traits such as fruit yield, fruit diameter, fruit length and fruit weight. The high diversity in the collection showed its great potential for improving horticultural traits in cape gooseberry.

Key words: Genetic divergence, multivariate analysis, Cape gooseberry, *Physalis peruviana*

Cape gooseberry (*Physalis peruviana* L.) is a minor fruit, usually cultivated as an annual and become perennial in the absence of frost. Pollination in this crop is predominantly autogamous, however some degree of out crossing takes place in the presence of pollinators insects like bees (Mc Cain, 1993). Fruit is a berry with color of yellow –orange, 1-3.5 cm diameter, very juicy, aromatic with a peculiar bitter-sweet flavor, enclosed by the acrescent epicalyx, which gives them the shape of bladder. The fruit can be eaten raw, as a dessert, an appetizer or used for dish decoration and preparation of elaborated dishes, in cakes or used for making jam (National Research Council, 1980). It is rich in vitamin A, B_1, B_2, B_{12}, C and poly phenols (Branzati and Manaresi, 1980; Sarangi *et al*., 1989).The commercial interest in this fruit has grown due to its nutritional properties related to high vitamin content, minerals and anti oxidants as well as its anti-inflammatory, anti-cancer and other medicinal properties (Yen *et al*., 2010; Me *et al*., 2009; Martinez *et al*., 2010). In spite of its great potential in respect of production and market acceptability, yet this fruit has not exploited for inclusion in the main stream of cultivated fruits. Since, it is a self-pollinated crop with narrow genetic base, the precise study of cape gooseberry germplasm available in the natural habitat shall boost the pace of improvement of this crop through various breeding devices. To evolve improved cultivars with better quality, information on association of quantitative and qualitative characters and study of genetic divergence among the available plant genetic resource is a vital tool for the plant breeders for an efficient choice of parents for plant improvement. Genetically diverse parents are likely to contribute desirable segregants and are expected to produce high heterotic crosses and therefore parents should be identified on the basis of divergence before taking any breeding program (Arunachalam, 1981). Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis' D^2-statistic has proved to be a powerful technique (Murty and Arunachalam, 1966). Cape gooseberry crop is well acclimatized and has great potential in temperate regions of India and having great variability, it needs to be identified, compared, selected and further explored for commercialization. Keeping in view these facts, the present studies were carried out to investigate the extent of genetic diversity in germplasm based on yield and quality traits using multivariate analysis.

*Corresponding author email: deshbsingh@yahoo.co.in

Materials and Methods

The study was carried out at the Research Farm of Central Institute of Temperate Horticulture (CITH), Srinagar, for two years i.e. from 2009-10 to 2010-11. Twenty genotypes of cape gooseberry (CITH CGB Sel- 1 to CITH CGB Sel- 20) collected from different

areas were taken for the study. The seedlings were transplanted in the month of May, 2010 for both the seasons at spacing of 30X30 cm. following randomized block design replicated three times and average data of two years were analyzed as per the method suggested by Gomez and Gomez (1984). Plant height (cm), fruit length (cm), fruit diameter (cm), fruit weight (g) and juices from the fruits for major chemical composition were measured. Acidity was determined by titration to pH 8.1 with 0.1M NaOH solution and expressed as percentage (AOAC, 1984). The total soluble solids (TSS) were determined with Atago digital refractrometer calibrated using distilled water. And results were reported as $_{o}$Brix at 22$_{0}$C. Ascorbic acid (mg/100 gm edible part) was determined by employing the method described by Ruck (1963). Genetic diversity was studied following Malanobsis's (1949) generalized distance (D_2) extended by Rao (1952). Clustering of genotypes was done according to Tocher's Method (Rao, 1952). Average intra-cluster distance was calculated by the following formula as suggested by Singh and Chaudhury (1985) .Trait variability analysis was performed by the PCA method, with the number of principal components being chosen based on the screen test (Kovacic, 1994). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes and as the Euclidean distance measure used was that best reflects differences existing among the genotypes (Kendall, 1980). All statistical analysis was carried out based on nine pomological and chemical traits using XL STAT-2011.

Results and Discussion

Data on variability parameters is presented in Table 1and the variability of each trait was expressed by standard deviation and the coefficient of variation. The lowest values of standard deviation were recorded in the cases of the titrable acidity (0.083) and the TSS $_{o}$brix (0.754). while it was highest for fruit yield (220.74). The coefficient of variation was lowest for the juice content (3.18%) followed by ascorbic acid (7.43%) while highest coefficient variation was found for yield (38.27%) and fruit weight (32.34%). The D_2 value estimates of genetic divergence for the cape gooseberry genotypes suggested in to four distinct clusters (Table 2) with wide range of diversity in the experimental material for majority of characters including the chemical traits (Fig 1). Cluster III consisted of a maximum of 10 genotypes (50%), cluster I consisted 4 genotypes (20%), cluster II consisted 2 genotypes (10%) and cluster I consisted only 4 genotypes (20%).the distribution pattern of different genotypes in to different clusters was apparently random and suggesting that germplasm collected from same geographic area are not necessarily closely related and different regions did not necessarily have different genetic background and being spread in the country. These results are in accordance with the findings of Gadekar *et al*,(1992) and Rai *et al*

Table 1. Variability for different traits in Cape gooseberry

Traits	Range		Mean*	St. dev.	CV (%)
	Minimum	Maximum			
No of fruit per plant	26.00	73.00	52.73	14.17	26.87
Fruit Weight (g)	6.51	19.10	11.10	3.59	32.34
Fruit length (mm)	20.24	29.82	23.66	2.81	11.89
Fruit diameter (mm)	23.06	34.22	27.52	3.65	13.27
Juice (%)	56.20	63.17	60.10	1.91	3.18
TSS ($_{o}$Brix)	6.92	9.71	8.58	0.754	8.78
Acidity (%)	0.280	0.670	0.517	0.083	16.04
Ascorbic (mg/100g edible part)	19.54	24.36	21.56	1.60	7.43
Fruit yield/plant (g)	199.67	1145.03	576.75	220.74	38.27

*Mean, arithmetic mean; st. dev., standard deviation; CV, coefficient of variation; min-minimum value; max-maximum value

Table 2. Distribution of different genotypes in to various clusters based on agglomerative hierarchical clustering analysis

S.No.	Cluster	No.of genotypes	Percent sharing	Name of genotypes
1	I	4	20	CITH Sel-1, CITH Sel- CITH Sel-3, CITH Sel-12, CITH Sel-13
2	II	2	10	CITH Sel-2, CITH Sel-20
3	III	10	50	CITH Sel- 4, CITH Sel- 5, CITH Sel-11, CITH Sel- 18, CITH Sel-8, CITH Sel-7, CITH Sel-13, CITH Sel-15, CITH Sel- 17, CITH Sel- 18
4	IV	4	20	CITH Sel-6, CITH Sel-17, CITH Sel-19, CITH Sel-9

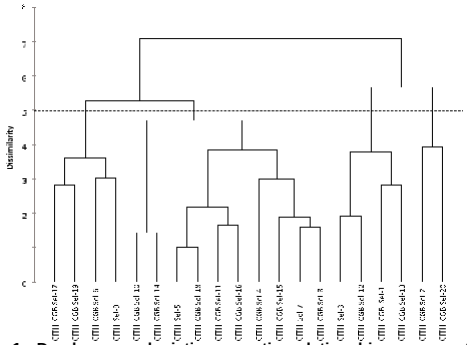

Fig.1. Dendrogram depicting genetic relationships among 20 cape gooseberry genotypes based on pomological and chemical traits produced by complete linkage analysis; (scale: Euclidean distance).

Table 3. Average intra- (bold face) and inter-cluster distance (D_2) for 20 Cape goose berry genotypes

Cluster	I	II	III	IV
I	120.93	539.76	179.20	117.38
II		159.93	716.54	424.15
III			81.34	292.51
IV				116.38

(1998) in tomato. While considering the inter cluster distances (Table 3), it was found that minimum (117.38) inter cluster distance was noticed between cluster I and IV. Thus crossing of genotypes from these two clusters may not produce better genotypes through hybridization. Maximum inter cluster distance (716.54) was noticed between cluster II and III genotypes which can be utilized for hybridization to generate useful recombinants in the segregation populations. Increasing parental distance implies a greater number of constraining

Table 4. Cluster means for nine characters in 20 Cape gooseberry genotypes

Traits	Cluster			
	I	II	III	IV
No. of fruit per plant	36.24	65.16	54.55	62.33
Fruit weight (g)	16.04	14.76	9.49	7.21
Fruit length(mm)	27.81	26.04	22.09	22.38
Fruit diameter (mm)	31.81	32.43	25.94	13.49
Juice %	61.75	60.24	59.15	62.42
TSS ((₀Brix)	8.80	7.73	8.89	7.10
Acidity (%)	0.545	0.352	0.545	0.460
Ascorbic acid (mg/100g edible part)	20.78	21.13	22.08	20.40
Fruit yield/plant (g)	589.15	985.30	526.00	447.88

alleles at the desired loci and these loci recombine in the F2 and F3 generations following a cross of distantly related parents leading to the greater opportunities for successful selection for any character of yield interest. Based on the cluster means from the Table 4, the important cluster was II for fruit per plant, fruit diameter, low acidity and fruit yield/plant. Cluster I for fruit weight and fruit length. Cluster III for TSS and ascorbic acid and cluster IV for juice content. From the results it was concluded that highest number of fruits per plant, fruit diameter and fruit yield, low acidity from cluster II, genotypes for higher fruit weight and fruit length from cluster I, cape gooseberry genotypes for higher TSS and ascorbic acid from cluster III and genotype for juice content from cluster IV could be selected as parents for hybridization programme. In accordance with these above Rahman and Mansur, (2009) also indicated that accessions among the cluster separated by high D_2 values could be used in hybridization program for obtaining wide spectrum of variations among the segregates. However, for a practical plant breeder, the objective is not only obtaining high heterosis but also to achieve high level of production with the shortest possible time. In the present study, the maximum distances existed between cluster II and cluster III. Considering group distance and other physico-chemical performance, the inter-genotypic crosses between the members of cluster II with that of cluster III are expected to exhibit high heterosis and is also likely to produce new recombinants with desired traits. Similar kind of results were also reported in tomato by Sharma and Verma (2001).

Table 5. Eigen values and proportion of variance explained by 10 principal Components

Principal component	Eigen value	Difference	Variability (%)	Cumulative %
PC1	3.453	1.59	38.365	38.365
PC2	1.861	0.29	20.678	59.043
PC3	1.563	0.646	17.371	76.414
PC4	0.917	0.308	10.193	86.607
PC5	0.608	0.132	6.760	93.368
PC6	0.476	0.400	5.293	98.661
PC7	0.076	0.050	0.846	99.507
PC8	0.026	0.007	0.289	99.796
PC9	0.018		0.204	100.000

Therefore, more emphasis should be given on cluster II and III in selecting inbreeds for crossing in cape gooseberry hybridization programmes. Eigen value of principal component axes of total variation obtained from principal component analysis are presented in Table 5. The results revealed that the first principal component largely accounted for the variation among the cape gooseberry genotypes (38.36%) followed by second principal component (20.67%) and third (17.37%). The first three principal components accounted (76.41%) of the total variation among nine characters describing twenty cape gooseberry genotypes, while the first two accounted (59.04%). The traits which contributed more positively to PC1 were fruit weight, length and diameter, while remaining traits in this PC1 did not contributed rather their effects were distributed

Table 6. Latent vectors for nine traits of 20 Cape gooseberry genotypes

Traits	PC1	PC2	PC3
No. of fruit per plant	-0.027	0.657	-0.205
Fruit weight (g)	0.511	-0.169	-0.116
Fruit length (cm)	0.493	-0.171	0.080
Fruit diameter (cm)	0.504	-0.116	-0.147
Juice (%)	0.190	-0.124	0.555
TSS (₀Brix)	-0.091	-0.323	-0.493
Acidity (%)	-0.178	-0.476	-0.176
Ascorbic acid (mg/100g edible part)	-0.028	-0.076	-0.513
Fruit yield/plant (g)	0.405	0.381	-0.266

among other PCs. The genotypes in the PC1 were more likely to be associated with higher fruit weight, fruit diameter and fruit yield whereas the genotypes with higher number of fruits per plant with low fruit weight and size were contributing to second PC (Table 6, Fig 2). The selected genotypes on the basis of different groups could be identified for yield potential. The PC3 showed that juice content was more positively associated than any other characters. The characters contributed positively to first three principal components could be given consideration while selecting the best genotypes without losing yield potential. When PC1 was plotted against PC2, some groups and some isolated genotypes were clearly defined viz. CITH CGB -20, CITH CGB -2, CITH CGB -9 and CITH CGB- 13

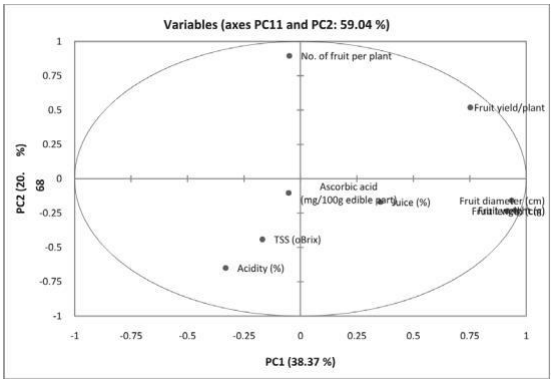

Fig. 2. Plot for 1st and 2nd PC for nine pomological and chemical traits in 20 genotypes of Cape gooseberry

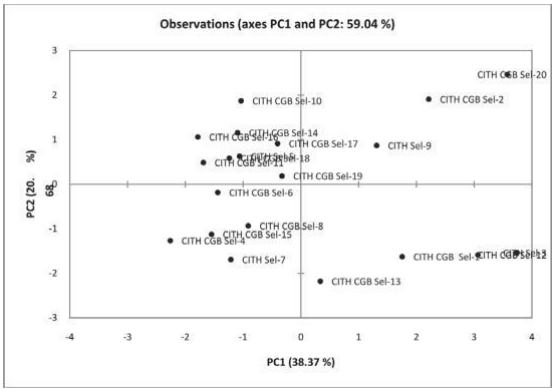

Fig. 3. Plot for 1st and 2nd PC for 20 genotypes of Cape gooseberry based on nine physic-chemical traits

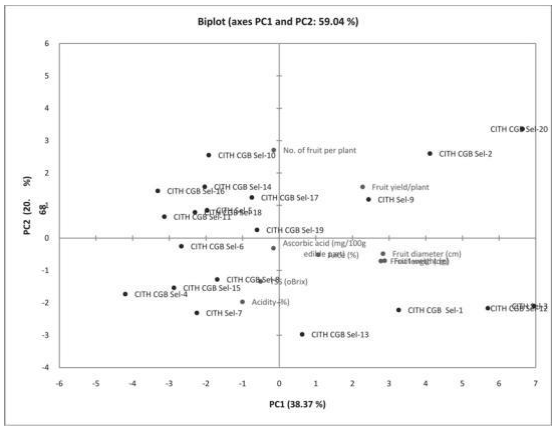

Fig 4- Biplot for 1st and 2nd PC for nine nine pomological and chemical traits in 20 genotypes of Cape gooseberry

(Fig 3). The biplot between PC1 against PC2 depict the combine results of correlation among the variable and diversity among the genotypes (Fig 4).

This grouping pattern confirmed the results obtained by D^2 analysis and that the crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture. The results of present study are thus useful as it gives information about the groups where certain traits are more important allowing breeder to conduct specific breeding programme.

References

AOAC, 1984. Official Methods of Analysis, 14th ed. Association of Official Analytical Chemists, Washington DC, U.S.A.

Arunachalam, G. 1981. Genetic distances in plant breeding. *Indian J. Genet*., **41**: 226-236

Branzati, E.C. and Manaresi, A. 1980. *L.alchechengi. Fruiticoltura* **42**: 59-63

Godekar, D.A., Dhanukshe, B.L. and Patil, F.B. 1992. Studies on variability, heritability and genetic advance in tomato. *J. Maharasthra Agric. Univ.,* **17**: 305-306.

Gomez, K.A. and Gomez, A. A. 1984. Statistical Procedures for Agricultural Research, 2nd Edn., John Wiley and Sons Inc., New York.

Kendall, M. 1980. Multivariate Analysis (Second Edition). Charles Griffin and Co., London.

Kovacic, Z. 1994. Multivariate analysis. Faculty of Economics. University of Belgrade. (In Serbian). p.293.

Martinez, W., Ospina, L.F., Granados, D. and Delgado, G. 2010. In vitro studies on the relationship between the anti-inflammatory activity of *Physalis peruviana* extracts and the phagocytic process. *Immuno Pharmacol Immunotoxicol,* **32**: 63-73.

Mc Cain, R.1993. Golden berry, passion fruit & white sapota: potential fruits for cool subtropical areas. J. Janick. J.E.Simon, Editors, New Crops, Wiley & sons, New York, pp.497-486.

Murty, B.R. and. Arunachalam, V. 1966. The nature of genetic divergence in relation to breeding system in crop plant. *Indian J. Genet*. **26**: 188-198.

National Research Council. 1989. Lost crops of incas: little known plants of the andes with promise for worldwide cultivation. Washington. DC: National academy press

Rahman, M.M. and Munsur, Al, M.A.Z. 2009. Genetic divergence analysis of lime. *J. Bangladesh Agril. Univ*., **7**: 33–37, 2009

Rai, N., Rajaput, Y.S. and Singh, A.K. 1998. Genetic divergence in tomato using non- heirarchical clustering approach. *Vegetable Sci*., **25** : 133-135.

Rao, C.R. 1952. Advanced Statistical Methods in Biometrics Research. John Wiley and Sons, New York, pp. 357-369.

Ruck, J.A. 1963. Chemical Methods of Analysis of Fruits and Vegetables. Department of Agriculture Canada, Publication No. 1154.

Sarangi, D., Sarkar, T.K., Roy, A.K., Jana, S.C. and Chattopadhyay, T.K. 1989. Physico-chemical changes during growth of cape goosebery fruit (*Physalis peruviana* L.). *Prog. Horti.* **21**: 225-228

Sharma, K.C. and Verma, S. 2001. Analysis of genetic divergence in tomato. *Ann. Agric. Res*., **22**: 71-73

Singh, R.K. and Choudhary, B.D. 1985. Diametrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, p. 318

Wu, S.J., Chang, S.P, Lin, D.L, Wang, S.S and Hou, F.F. 2009. Supercritical carbon dioxide extract of *Physalis peruviana* induced cell cycle arrest and apoptosis in human lung cancer H661 cells. *Food Chem. Toxicol*..

Yen, C.Y., Chiu, C.C, Chang, F.R, Chen, J.Y and Hwang, C.C. 2010. 4beta-Hydroxywithanolide E from *Physalis peruviana* (golden berry) inhibits growth of human lung cancer cells through DNA damage, apoptosis and G2/M arrest. *BMC Cancer,* **10**: 46.

Received: June 6, 2012; Revised: September 28, 2012; Accepted: February 11, 2013